



Replacement Sheet

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1 GTCCCTCCACCATGCACTCGCTGGGCTTCTCTCTGTGGCGTGTCTCTCTGCTCGCCGCTG 60
-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGGTACGTAGCGACCCGGAAGAAGAGACACCCGACCAAGAGACGAGCGGCGAC
M H S L G F F S V A C S L L A A A -
CGCTGCTCCGGGTCTCGGAGGCGCCCGCGCGCGCGCGCTTCGAGTCCGGACTCG 120
-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGCCCCAGGAGCGCTCCGCGGCGGCGGCGGCGGGAAGCTCAGGCCCTGAGC
L L P G P R E A P A A A A A F E S G L D -
ACCTCTCGGACGCGGAGCCCCGACGCGGCGGAGGCCACGGCTTATGCAAGCAAAGATCTGG 180
-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCTCGGCGTGGCGCCCGCTCCGGTGCCGAATACGTTCGTTCTAGACC
L S D A E P D A G E A T A Y A S K D L E -
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT 240
-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y -
ATTGGAATAATGTACAAGTGTGCTAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG 300
-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTACATGTTACAGTCGATTCTCTTCTCCGACCGGTGTGATTTGTCTCTTGTTCC
W K M Y K C Q L R K G G W Q H N R E Q A -
CCAACCTCAACTCAAGGACAGAGACTATATAAATTTGCTGCAGCACATTATAATACAG

FIG. 1A



Replacement Sheet

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TTTACAGACAAGTTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720
-----+-----+-----+-----+-----+-----+-----+
AAATGCTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG
Y R Q V H S I I R R S L P A T L P Q C Q -
AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780
-----+-----+-----+-----+-----+-----+-----+
TCCGTCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTCTACGG
A A N K T C P T N Y M W N N H I C R C L -
TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840
-----+-----+-----+-----+-----+-----+-----+
ACCGAGTCCTTCTAAATAACAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D S T D G F H -
ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTCAGTGTCTGCAGAG 900
-----+-----+-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCAACACAGACGTCTC
D I C G P N K E L D E E T C Q C V C R A -
CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAAACTCATGCCAGT 960
-----+-----+-----+-----+-----+-----+-----+
GCCCCGAAGCCGACGGTCCGACACCTGGGGTGTCTCTTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C -
GTGTCTGTAAAAACAACACTCTTCCCCAGCCCAATGTGGGGCCCAACCGAGAAATTGATGAAA 1020
-----+-----+-----+-----+-----+-----+-----+
CACAGACATTTTGTGTTGAGAAGGGGTCGGTTACACCCCGGTGGCTCTTAAACTACTTT

FIG. 1C



V C K N K L F P S Q C G A N R E F D E N -
ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080
-----+-----+-----+-----+-----+-----+-----+
TGTGTACGGTCACACATACATTTCTTGACGGGCTCTTTAGTTGGGATTTAGGACCTT
T C C Q C V C K R T C P R N Q P L N P G K -
AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC 1140
-----+-----+-----+-----+-----+-----+-----+
TTACACGGACACTTACATGTCTTTTCAGGTGTCTTTACGAACAATTTTCCCTTTCTTCAAGG
C A C E C T E S P Q K C L L K G K K F H -
ACCACCAACATGCAGCTGTTACAGACGGCCCATGTACGAACCGCCAGAAAGGCTTGTGAGC 1200
-----+-----+-----+-----+-----+-----+-----+
TGGTGGTTTGTACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACTCG
H Q T C S C Y R R P C T N R Q K A C E P -
CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCATATTGGCAAAGACCAC 1260
-----+-----+-----+-----+-----+-----+-----+
GTCCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
G F S Y S E E V C R C V P S Y W Q R P Q -
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAAAAGTGTGT

FIG. 1D



Replacement Sheet

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1261 -----+-----+-----+-----+-----+-----+-----+ 1320
TTTACTCGATTCTAACATGACACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGTGACACA
M S *
TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTGGTGCCATGCTAACAAAGACA 1380
1321 -----+-----+-----+-----+-----+-----+-----+
ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT
AAAGTCTGTCTTTCCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG 1440
1381 -----+-----+-----+-----+-----+-----+-----+
TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC
CAAAAGGCCCTCTTGTAAGACTGGTTTCTGCCAATGACCAACAGCCAAGATTTTCCTC 1500
1441 -----+-----+-----+-----+-----+-----+-----+
GTTTCCGGAGAACATTCTCTGACCACAAAGACGGTTACTGGTTGTCTGGTTCTTAAAGGAG
TTGTGATTCTTTAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGTC 1560
1501 -----+-----+-----+-----+-----+-----+-----+
AACACTAAAGAAAATTTTCTTACTGATATATAATAAAGGTGATTTTATAACAAAGACG
ATTCATTTTATAGCAACAACAAATTGGTAAAACTCACTGTGATCAATAATTTTATATCAT 1620
1561 -----+-----+-----+-----+-----+-----+-----+
TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA
GCAAAAATATGTTTAAAAATAAAAATGAAAATTTGTATTTATAAAAAAAAATAAAAA 1674
1621 -----+-----+-----+-----+-----+-----+-----+
CGTTTATACAAAATTTTATTTTACTTTTAAACATAAATATTTTTTTTTTTTTTTTTTT

FIG.1E